

10048024 Results

SEQ ID NO: 1

RESULT 16

AAW84306

ID AAW84306 standard; peptide; 27 AA.

XX

AC AAW84306;

XX

DT 18-MAR-1999 (first entry)

XX

DE Finger 3 of a NABP specific for a G12V mutant ras oncogene.

XX

KW Zinc finger; nucleic acid binding protein; NABP; ras oncogene mutant;

KW Cys2-His2 zinc finger; detection; gene therapy; gene delivery.

XX

OS Synthetic.

XX

PN WO9853059-A1.

XX

PD 26-NOV-1998.

XX

PF 26-MAY-1998; 98WO-GB001514.

XX

PR 23-MAY-1997; 97GB-00010807.

XX

PA (MEDI-) MEDICAL RES COUNCIL.

XX

PI Choo Y, Klug A, Isalan M;

XX

DR WPI; 1999-045308/04.

XX

PT Preparation of nucleic acid binding proteins - by designing protein

PT sequences of a Cys2-His2 zinc finger class based on a nucleic acid base

PT triplet in a target nucleic acid sequence.

XX

PS Example 4; Fig 5C; 62pp; English.

XX

CC The present sequence represents finger 1 of a nucleic acid binding
 CC protein (NABP) specific for a G12V mutant ras oncogene. The specification
 CC describes a method for preparing a NABP of the Cys2-His2 zinc finger
 CC class capable of binding to a nucleic acid base triplet in a target
 CC nucleic acid sequence. Binding to the 5' base of the triplet by an alpha-
 CC helical zinc finger nucleic acid binding motif in the protein is
 CC determined as follows: (a) if the 5' base in the triplet is A, then
 CC position +6 in the alpha-helix is Glu, Asn or Val; (b) if the 5' base in
 CC the triplet is C, then position +6 in the alpha-helix is Ser, Thr, Val,
 CC Ala, Glu or Asn. The methods can be used for designing a protein which is
 CC capable of binding to any predefined nucleic acid sequence. The NABPs can
 CC be used for the detection of target nucleic acid molecules. They can also
 CC be used in gene therapy, e.g. for the delivery of functional genes into
 CC defective genes, or the delivery of nonsense nucleic acid to disrupt
 CC undesired nucleic acid

XX

SQ Sequence 27 AA;

Query Match 4.2%; Score 7; DB 2; Length 27;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 HTRTHTG 115
 |||||
 Db 19 HTRTHTG 25

RESULT 17

AAW78389

ID AAW78389 standard; peptide; 27 AA.

XX

AC AAW78389;

XX
 DT 11-MAY-1999 (first entry)
 XX
 DE Finger #3 of zinc finger targeted to mutant H-ras coding sequence.
 XX
 KW Zinc finger; target sequence; binding assay; mutant;
 KW phosphorylation site; functional domain.
 XX
 OS Synthetic.
 XX
 PN WO9853060-A1.
 XX
 PD 26-NOV-1998.
 XX
 PF 26-MAY-1998; 98WO-GB001516.
 XX
 PR 23-MAY-1997; 97GB-00010809.
 XX
 PA (MEDI-) MEDICAL RES COUNCIL.
 XX
 PI Choo Y, Klug A, Isalan M;
 XX
 DR WPI; 1999-045309/04.
 XX
 PT Rules for designing zinc finger nucleic acid binding proteins specific
 PT for any base quadruplet - relate bases in the quadruplet to specific
 PT amino acids in the alpha-helical binding motif, used to detect target
 PT nucleic acids, e.g. for identification of mutants and phosphorylation
 PT sites.
 XX
 PS Example 1; Fig 1C; 57pp; English.
 XX
 CC This sequence represents finger #3 from a synthesised zinc finger
 CC targeted to the mutant coding sequence for amino acids 8-16 of the H-ras
 CC oncogene (AAAX16975). The synthesised zinc finger belongs to the Cys2-His2
 CC zinc finger (ZF) class (AAW78382). The ZF are generated so that they are
 CC able to bind a nucleic acid quadruplet in a target sequence, where binding to
 CC base 4 of the quadruplet by an alpha-helical ZF binding motif is
 CC determined as: (a) if base 4 is A, then position +6 in the helix is Gln
 CC and position ++2 is not Asp (++2 indicates a residue present in an
 CC adjacent, C-terminal ZF) and (b) if base 4 is C, then position +6 may be
 CC any residue provided ++2 is not Asp. The ZF are used to detect target
 CC nucleic acids in a binding assay, e.g. for identification of mutants
 CC (they can differentiate between single bp changes in the target) or
 CC potential phosphorylation sites, and to characterise functional domains
 CC of a protein
 XX
 SQ Sequence 27 AA;

Query Match 4.2%; Score 7; DB 2; Length 27;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 HTRTHTG 115
 |||||
 Db 19 HTRTHTG 25

RESULT 18

AAW84305
 ID AAW84305 standard; peptide; 28 AA.
 XX
 AC AAW84305;
 XX
 DT 18-MAR-1999 (first entry)
 XX
 DE Finger 2 of a NABP specific for a G12V mutant ras oncogene.
 XX
 KW Zinc finger; nucleic acid binding protein; NABP; ras oncogene mutant;
 KW Cys2-His2 zinc finger; detection; gene therapy; gene delivery.
 XX

OS Synthetic.
 XX
 PN WO9853059-A1.
 XX
 PD 26-NOV-1998.
 XX
 PF 26-MAY-1998; 98WO-GB001514.
 XX
 PR 23-MAY-1997; 97GB-00010807.
 XX
 PA (MEDI-) MEDICAL RES COUNCIL.
 XX
 PI Choo Y, Klug A, Isalan M;
 XX
 DR WPI; 1999-045308/04.
 XX
 PT Preparation of nucleic acid binding proteins - by designing protein
 PT sequences of a Cys2-His2 zinc finger class based on a nucleic acid base
 PT triplet in a target nucleic acid sequence.
 XX
 PS Example 4; Fig 5C; 62pp; English.
 XX
 CC The present sequence represents finger 1 of a nucleic acid binding
 CC protein (NABP) specific for a G12V mutant ras oncogene. The specification
 CC describes a method for preparing a NABP of the Cys2-His2 zinc finger
 CC class capable of binding to a nucleic acid base triplet in a target
 CC nucleic acid sequence. Binding to the 5' base of the triplet by an alpha-
 CC helical zinc finger nucleic acid binding motif in the protein is
 CC determined as follows: (a) if the 5' base in the triplet is A, then
 CC position +6 in the alpha-helix is Glu, Asn or Val; (b) if the 5' base in
 CC the triplet is C, then position +6 in the alpha-helix is Ser, Thr, Val,
 CC Ala, Glu or Asn. The methods can be used for designing a protein which is
 CC capable of binding to any predefined nucleic acid sequence. The NABPs can
 CC be used for the detection of target nucleic acid molecules. They can also
 CC be used in gene therapy, e.g. for the delivery of functional genes into
 CC defective genes, or the delivery of nonsense nucleic acid to disrupt
 CC undesired nucleic acid
 XX
 SQ Sequence 28 AA;

Query Match 4.2%; Score 7; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 109 HTRTHTG 115
 |||||
 Db 19 HTRTHTG 25

SEQ ID NO: 5

RESULT 7
 I66494/c
 LOCUS I66494 7218 bp DNA linear PAT 28-DEC-1997
 DEFINITION Sequence 14 from patent US 5670367.
 ACCESSION I66494
 VERSION I66494.1 GI:2724471
 KEYWORDS .
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 7218)
 AUTHORS Dorner, F., Scheiflinger, F. and Falkner, F. Gunter.
 TITLE Recombinant fowlpox virus
 JOURNAL Patent: US 5670367-A 14 23-SEP-1997;
 FEATURES Location/Qualifiers
 source 1..7218
 /organism="unknown"
 /mol_type="unassigned DNA"
 ORIGIN

Query Match 5.5%; Score 72; DB 6; Length 7218;
Best Local Similarity 8.3%; Pred. No. 3.7e-10;
Matches 33; Conservative 214; Mismatches 149; Indels 0; Gaps 0;

```
Qy      911 ACAGTGCACAAGTCAGGAGACCTAGGTCTACTCTGCACTTGCTAATTAGCTCTATG 970
          || ||| || || | | ||| | | | | | | | | | |
Db      1504 AACGGCATGTAGGCATCACTGTAATTACCTATCTATGCAAGTAGTTAAAGAGATAGAAG 1445

Qy      971 ACTCTGGGCAAATCGCATATCTGGGCCTCAGTTTCTCTATCTGTAAAAATGACAGCAAAC 1030
          || ||| : : : : : : : : : : : : : : : :
Db      1444 AATTTGGTACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1385

Qy      1031 TCGTAATGCTCAATAAATGTTTAAATAACAACGAAAAGAAAGAAACCAAGTCAGGCGAC 1090
          : : : : : : : : : : : : : : : : : : : :
Db      1384 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1325

Qy      1091 AAGGAGCGTAGAACAGACCAAACGAGGCGGCCGCGAAGGAGACGGAAGCCAGGTGTGGG 1150
          : : : : : : : : : : : : : : : : : : : :
Db      1324 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1265

Qy      1151 CGAGGAGTAAGAAGAGGGGGCGCGCAGCCCGAAATAAGGTTGCAAGACCAGCGACCGAG 1210
          : : : : : : : : : : : : : : : : : : : :
Db      1264 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1205

Qy      1211 AGATAGATATACAGAGAGCCGAGCGAAGAGCACGCGAGCACACAGCCTCCGCTCCAGCC 1270
          : : : : : : : : : : : : : : : : : : : :
Db      1204 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1145

Qy      1271 GAAGAGAGGGCAGCTAACAAGAAGAAACGCAGATGA 1306
          : : : : : : : : : : : : : : : : : : : :
Db      1144 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1109
```

RESULT 1

US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300

